

Figure 2: Nucleotide sequence of TbF15
Sheet 2 of 4

TCTCTGGCCCTTTGCTGGCTTGTCACTGTTCTGCGTTATCCCCGATTCTGCGAT
AACCCTATTAACGCCCTTGAGCTGAGCTGATACCGCTCGCCGAGCCGACCGAGCCAGCGAG
TCAGTGGAGCAGGAAGGGAGAGCCCTGATGGCTTAITTCCTCTAGGCATCTGCGGATT
TCACACCGCATATACTGGTCACTCTAGAATCTGCTCATGGCTGGGCCCGACACCCGCA
CACTCCGCTATCCTACGGTCACTGGTCACTGGCTGGGCCCGACACCCGCA
GCCCCTGACGGGCTTGTCTCCGGCATCCGCTACAGACAGCTGTGACCGCTCCGGAGCTG
CATGTGTCAGGGTTTCAACGGCTCATCACGAAACCCGGAGGAGCAGCTGCGGTTAAGCTCATCAGG
CTGGCTGTGAGCGATTCAACRGATGCTGCTGGTCTACCGCCTCACAGCTGTTAGGTTCTCCAG
AAGCGTTAATGCTGCGCTGTGATAAACGGCCGATGTTAAGGGGGTTTCTCTGTTGGTCA
TGATGCTCTGGTAAAGGGGATTCTGTTATGGGTTAATGTAACCGATGAAACGAGAGGGAT
GCTCACGGATACGGTTACTGATGATGAACTGCCCCGTTACTGGAACAGCTGTGAGGTTAAACACT
GGGGCTGATGGATGCGGGGCCAGAGAAAARTACTCAGGTCAATGCCAGGCTTGTGTTAAAC
AGATGTTAGGTTCTCCACAGGGTAGCCAGGACCATCTGCGATCACAGCTGGAAACATTAATGGTGC
GGGGCTGACTTCCGGTTTCCAGACTTACGAAACGGAAACCGGAAGACCATTCATGTTGTC
TCAGGTCGAGACCTTNTGAGCAACGACTGCTCTGGTCTCGCAGTATGGTTATCCTG
CTAACCGATAGGCAACCCGGCACGCTAGCCGGGTTCTACGGGCTTCTACGGAGCA
CGTGGGGGGCCCATGCGGQATAATGGCTGCTCTCGGGAAACGTTGGGGGGGACAGT
GAGGAAGGGCTTGAAGGGGGGTGCAAGGTTCCGAAATACCGCAAGCGACAGGGCGATCATGTCG
GCTCCAGGQAAGGGTCTCGGGAAATGACCCAGGGCTGCGGGACCTGCTTACAGGTTG
CATGATGAAAGAGACAGTCATAGTGGCGGAGGATATGCTACGGGCGGGGACCGGAGGCT
GACTGGGTTGAAGGCTCTCAAGGGCATCGGCGATGGCTGACATGGCTGAGTQACCTAACTTAC
ATTAATTGGCTGCGCTCATGCCCTTCTGCGGAAACCTGCTGCGCAGCTGCAATTATG
ATTCGGGCCRACGCCGGGGAGAGGCGTTNGGTTATGGGGCGCAGGGTTTTTCTTACCCA
GTGAGACGGCAACAGCTGATGGCTCTACGGCTGGGCTTCTGAGAGACTTGCAAGCAGGGCTCA
CGCTGGTTTGGCCGAGGGAAATCTGGTGGTGGTGGTAAACGGGGGATAATACAGG
TGTCTCGGATAGTGTGATACCAACTACGGAGATATCGCACCARCGCCAGCCGGACTCGGIAA
TGGCGCGCATGGCGCCAGGCCATCTGTCGTTGGCAACGAGCATCGCACTGGGAGGATGECCT
CATTCAGGATTTGCTGGTTGGTGGAAACCGGACATGGCACTCCAGCTGCGCTTCCGGTCTGCTA
TGGGCTGTAATTGCGAGTGGATATTTGCTGGTGGTGGTAAACGGGGGATAATACAGG
AACTTAATGGGGCCGCTAACAGCGCGATTTGCTGGTGGTGGCAACCGGAGGAGCAG
GTGCGGTACCGTCTCATGGGAGAAAATAACTGTTGATGGGTTCTGGTCAAGAGACATCAAGAA
ATAACGGGGAAACATTAGTCAGGCGAGCTTCCACAGCAATGGCATCTGGTCACTCGGGAGTGT
TAATGATCACGCCACTGGCGGTTGGCGAGAGATTGGTGGCAGCCGGCTTACAGGCTCGACG
CGCTCTGGTTTACCATGCAACCCAGGGCTGGCAGACTGGAGGTTGGCAACGCCAATCAGGAA
CGACTTGGCGATGGTGGCAGGGGGAGTGTAACTTGCCTGGCAGCTGCCCATCGGGCTTCC
TGCCCCGGCATGGTGGTGGCAGGGGGAGTGTAACTTGCCTGGCAGCTGCCCATCGGGCTTCC
TTTCCCGGGCTTTCGCAAAAACCTGGCTGGCTGGCTGGTACCCAGGGGAAACGGCTGATAAGAGA
CACCGGCACTACTCTGGCGATCATGCAATTACGGCTTACTGGTTTACATCCACCGGCTTACAGG
CTGGGGGGGGCTATCATGGCATACCGCAAAAGGGTTTGCGCCATTGCACTGGTGTGCGGGATCTGA
CGCTCTCCCTTATGGCAGCTGCACTGGAGAGCTGGCGGACAGTGGCCGAGGACCT
GCCCGCGCAAGGAAATGGTGGCGATGGAGAGATGGCGGCCACAGTGGCCGAGGACCT
ACCATACCCACCGGCAACAGGCTCATGGCGGAGATGGCGGCCACAGTGGCGAGGCCGATCT
ATGGTGGCGATATAGGGGGCAGCAACCGCACCTGTGGCGGGGTGATGCCGGCAAGATGCGCTCG

Figure 2: Nucleotide sequence of TbFl5
Sheet 3 of 4

Figure 2: Nucleotide sequence of TbF15
Sheet 4 of 4

CGGGCCCCGCTGGCGCTGGTGACATTGCCGGCTTAGGCCAGGGARGGGCCGGCGGGCGCCGCGCT
GGGCGGGCGGTGGCATGGGAATGCCGATGGGTGCCGCATCAGGGACAAGGGGGCCCAAGTCAA
GGTTTCAGCAGGAAGAACGAGGGCGCTCTACACCGAGGGATCGGGCATGGACCGAGGCCGTCATTGG
TAACCGTGGCGCCAGGACAGTAAGGAGTCGAACTGAAATTCTGCAGATAATCCATCACACTGGCGC
CGCTCGAGCACCCACCACCACTGAGATCGGGCTGCTAACAAAGCCGAAAAGGAAGCTGAGT
TGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGCCTCTAAACGGGTCTTGAGGG
GTTTTTGCTGAARGGAGGAACATATCCGGAT

Figure 3: Amino Acid Sequence of TbF14

MQHHHHHHHTDRSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQALLNARDE
LQAQIDKWRRRVIEPIDMAYRQFLTEIGYLLPEPPDFTTTSGVDAEITTTAGPQLVVPVLNAR
FALNAANARWGSLYDALYGTDVIPETDGAEKGPFTYNKVRGDKVIAYARKFLDDSVPLSSGSFGQDAT
GFTVQDGQLVVALPDKESTGLANPGQFAGYTGAESPTSVLLINHGLNIEIILIDPESQVGTDRAGV
KDViLESAITTIMDFEDSVAAVDAADKVLYGRNWLGJNKGDLAIAAVDKDGTAFRLVLRNDRNVTAP
GGGQFTLPGRSILMPVNRVGHLMTMDAIVDTDGSVFEGIMDALFTCLIAIHGLKASDVNGPLINSR
TGSIYIVPKMHGPABEVFTCELSRVEDVLGLPQNTMKIGIMDEERRTTVMLKACIKAADRVVF
INTGFLDRTGDEIHTSNEAGPMVRKGTMKSQPWILAYEDHNVDAAGFSGRAQVGKGMWTTEL
MADMVETKIAQPRAGASTAWVSPTAATLHALNYHQDVPAVQQGLAGKRRATIEQLLTIPAKEL
AWAPDEIREEVDDNNCQSILGYVVRNVQGVGCSKVPDIHDVALMEDRATLRISSQLLANWLRCVGI
TSADVRASLERMAPLVDRQNAQGDVAYZPMPNFDDSTAFLAAQELILSGAQQPNGYTEPILHRRRR
EFKARAEEKPAKPSDRAGDDAARVQKYGGSSVADAERIRRVRAERIVATKKQGNNDVVVVSAMGDTTD
DLDDLAQQVCPPAPPRELDMLLTAGERISNALVAMATESELGAHARSFTGSQAGVTTGTHGNAKII
DVTGRLQTALEEGRVV/LVAGFPQGVSDQTKDVTTLGRGGSDDTTAVAMAALGADVCEIYTDVDGIF
SADPRIVRNARKLDTVTFEEMLEAACAKVLMRCVEYARRHNIPVHVRSSYSDRPGTVVVGSIK
DVPMEDPILTGVAHDRSEAKVTIVGLPDIPGYAAKVFRAVARRRRQHRHGAAERIQGRGRQDRHHL
HLLPOTSGPPPWNTRSETRSASTQILYDDHICKVSLIGAGMRSHPGVTATFCEALAAVGVNIEL
ISTSEDQRSRCCAATPNWTRPNSRCMRSGSAATRRPRCTRGRDGRWACQ..

Figure 4: Amino Acid Sequence of TbF15

MGGHHHHHHHIVIDIIGTSPTEWQAAAEEAVQRARDSVDDIRVARVIEQDMAVDSAGKITYRIKLEVSE
KMRPAQPRCGSKPPSGSPETGAGAGTVATTASSPVTLASTGSTLLYPLPNLWGPAFHERYPNVTI
TAQGTGSCAGIAQAAGTVNIGASDAYLSEODMAAHKGLMNIALAISAAQVNVNLPGVSEHLKLNG
KVLAAMYQGTIKTWDDPQIAALNPVGVLPGTAVVPLHRSRGSGDTFLFTQYLSKQDPECWGKSPGF
GTTVDFPAPVPGALGENGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQ
SIQAAAAGFASKTPANQAIMSDGPDGYPINYEYAIVNRRQKDAAATQTLQAFLHWAITDGNK
ASFLDQVHFQPLPPAVVVKLSDLALIATISSAEKTDAAITLAQEAGNFERISGDLKTQIDOVESTAGS
LGQQWEGRAAGTAAQAVVRQEAANKQKQELDEISTNIRQAGVQYSRADEEQQQQALSSQMGTQSQ
TVTVDQQETLNRAANEVEAPMDPTDVPITCPCELTAAKNAACQQLVLSADNMREYLAAGAKERORLA
TSLRNAAKAYGEVDDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPKVATAGEPNFMDLKKEAA
RKLETGDQGASLHNFADGWNTFNLTLGQDVKRFRGFDNWEGDAATACEASLDQQRWILHSMALKSA
AMAKQAOQVVAQLHVWARREHPTYEDIIVGLERLYAENPSARDQILPVYAELYQQRSEKVLTEYNKAA
LEPVNPPKPPPAIKIDPPPQQEQGLIPGFLMPPSDGSQVTPTGMPAAPMVPPGSSPGGGLPADT
AAQLTSAGREAAAALSGDVAVKAASLOGGGGGGVPSAPLGSAIGGAESVRPAGAGDIAGLGQGRAGG
GAALGGGGCMMPGAAHQGGGAKSKGSQQEDEALYTEDRAWTEAVIGNRRQDSKESK.

Figure 5

	Status	TbF15	TbF6
5004	TB	0.926	1.043
7004	TB	0.922	1.182
9004	TB	1.021	1.235
11004	TB	0.858	1.629
15004	TB	2.035	2.099
17004	TB	2.393	2.861
18004	TB	1.777	0.412
21004	TB	2.062	1.635
23004	TB	0.429	0.561
26004	TB	0.390	0.392
27004	TB	0.244	0.207
28004	TB	1.246	1.205
30004	TB	1.053	1.082
32004	TB	1.240	1.921
33004	TB	1.504	1.579
34004	TB	1.059	1.153
36004	TB	0.546	1.105
37004	TB	1.446	1.939
39004	TB	2.021	2.782
41004	TB	0.511	0.652
43004	TB	0.855	0.483
44004	TB	0.711	0.666
53004	TB	1.102	0.317
FD8-24	Control	0.183	0.314
FD8-25	Control	0.061	0.063
FD8-26	Control	0.066	0.142
FD8-27	Control	0.021	0.115
FD8-28	Control	0.053	0.289
FD8-29	Control	0.114	0.238
FD8-30	Control	0.105	0.146
FD8-31	Control	0.101	0.237
FD8-33	Control	0.080	0.071
FD8-34	Control	0.140	0.117
FD8-35	Control	0.088	0.072
FD8-36	Control	0.081	0.089
FD8-37	Control	0.057	0.06
FD8-38	Control	0.104	0.111
FD8-39	Control	0.221	0.241
FD8-40	Control	0.237	0.265
FD8-41	Control	0.056	0.093
FD8-42	Control	0.184	0.273
FD8-43	Control	0.126	0.126
FD8-44	Control	0.193	0.092
FD8-45	Control	0.058	0.057
FD8-46	Control	0.183	0.23
FD8-48	Control	0.062	0.085
FD8-49	Control	0.134	0.247
Mean		0.113	0.157
SD		0.061	0.086
Mean + SD		0.298	0.414
Sensitivity		22/23	20/23

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Wednesday, July 23, 1969 10:42 A.M.

在於一九三〇年，即為當時的「新詩」。

Quality Control Using Error-Prone Enzymes 2003

4878-4

CAGGCACTGAGGCAAGCGTTCGTCATGGAACTACAGGAACTTGCGAATGAGCAGG

CCCCATGCTTCAGAAGTACCCCTTGCTTGCGGTAACTGGAACTGGCTGGGTTGCACTGCTTCAGAAGTACCCCTTGCTTGCGGTAACTGGAA

HTCC-1.2.3 300nm

268

• KTCG-13

• MRCG-18

WTGG-15

2025 RELEASE UNDER E.O. 14176

RDIXKEGAXXKLEPFYRPRVAYQLTTEPTVYVNLISAA
CFFCGAGGCGCCGGTTFCGCGGGCGCGATGCCCTTGTCGCGCGGCTTTCGCTGCTGAAACGCTGTGATCGACGCCGCTGCAAGCTGCCTGAA
GAGGCTCGCGCGCAAAAGCTGCCCGCGCTTACCGCGTACGCCCGCGCGAACCCTGAGCAACGACTTGTGCGCTGATGTTGCGCTGAGTTCAGAGCTT
\$00

- KTCG-18 -

• HINDU FB

TCATGCAACGCCCTTCAAGGCGAAGACCTTGAGACGTCAGGGGTGGGTTGAACTGTTCTCTTGAGGCTGGTGAACATGGAGFCCTT
AGTAGTGTTGGCAGGACTTCCTGAACTCCCTGTCAGGTCCTGAACTGCTTCAACAGAGCFCCTGCGCTTGTGACTTCAGGAA

Digitized by srujanika@gmail.com

→ NTOC-1

sheet 1 of 2

Sunday July 26 1964 10:42 AM

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2002-01-00000000-01-00000000000000000000000000000000

20

NTCC → PL

CCGCGTCAACTCTGTAGGCGTACGGGCCGATAGTGTCGGGCGCGCTGGCGGAGCCTGGCGGAGCTGCGAGGTGTGTTGGCGGCGAGGT

100

RTGCO-1 FL

TTCCCCAAGGTATGGCGGACCGTATGCCGGCTTCACGGCTTCCTCGGCGGCTCGAAGGCGAACGCGCCGGAAAGTACTCAGAACGGCTG

10

HICG-1 E

HTDC-1 R.

504

Sheet 2 of 2

Tuesday, July 26, 1995 10:40 AM
TCC1(1-320) was msp (1 > 72%) Site 200 608
enzymes 212 of 314 enzymes (fibers)

Linear Correlation Filter with Sign-and-Gamma Cocks

FIG. 7.a

Wednesday, July 23, 1997 (0:50 AM)
ATCC1(1844392) MBD.mpc (51 - 881) S- 15-8 404

H765-1 (1344 - 3784)

二〇〇〇

FIG. 7b

Monday, July 23, 1996 10:48 AM
 FCC(1)-120 Map.MPD (1 > 411) 5 quences

enzymes: All 513 enzymes (no filter)

codons: Circular, Certain Start Only, Standard Genetic Code

ATGCAATACCATCACCATCALATGAGCAGAACGGTCACTAATGTCATAACAGATCAAGTGCGCTGTAGACGCTGTAGCGATTTG 92

TACGATGCTGATGGTAGCTGACTCGCGCTGCGAACTGAGTGGTAGGGTGCCTGATGCGCGGTAATCTCCGAACATGCTGAGAAGACCCGATCG 101

M K H H H H M S P A F I E Q P T I S A I G L Y C U L G I S

AATACCAACCCAGGGCTATGCCCTTACTCTGACFACACTCTGCGAACGGCTGGAGAGCTTGCGAGCGCTTTCGCGTGATGGCT 110

TCATGGTGGCTTCGCGATAGGAAATGAGCTGCTGATGAGGCTTTCGCGAGCTTCGCGAGCTTCGCGAGCTGCGCGATCTACCGA 119

I P N Q C G F L Y S S L E Y F E X A L E S L A A A R P P G O G

GTTTAQGCTTGGCGCCGAGCAAATACGCCCGCAAAACGCCAAACCAACGGTGAATTCTTCGAGGAACTGGCGAGCCGCGATCTCGAGCTCTAC 278

CCATATCCAAACGCCGGCTGTCTATGCTGCCGCTTGGCTGGCTGCGACTTAAARAAACGCTCTTCGCGACCTCTGCGAGCTGAGTAG 287

W L Q S A K O K Y A G R N R P N H Y N F F G E L A O L D R Q L A

AGKCTGATCCACCGAACGGCCGACGGCTGCGAGGACGGCGGCGACATCTGGAGGCGCCGAAAGAGGGCTTCGAGFFDTGCGCGCGCTGCG 368

TGGGACTAGGTGCTAGTCGGCTTUCGCCAGGCTGCTGGCTGGCTGGCTGGCTGCTGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 377

S L I N G O G A N A Y Q T T P D I L E S R X X G L E F V R P V A

TGTGGACCTGACCTGACATGCCGGCTGGCGAGCGCTATAG 411

ACACCTGGACTGGATGTAAGGCCAGCAAGCCGCGCGGGAGATAC

V O L T Y E P V V G H A L

HIGE-L (1-123)

Page 1

FIG. 7c

Sunday, July 28, 1996 10:00 AM
24inch x 36inch Class A 15 x 1809 9000 and 1000
newspaper AS ITS ENTIRETY AND PAPER

KG12-H7CC-1

2309

FIG. 8
Sheet 1 of 2

Wednesday, July 26, 1995 12:46 AM
5: Tenth FCC meeting (11 a.m.-12:30 p.m., Room 202 and 3)

235

FIG. B
Sheet 2 of 2

FIG. 9a

SEARCHED July 22, 1999 1:35 PM

TUESDAY, JULY 22, 1980 1:35 PM

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NTCC1

G G G Q L Y S A Q C S G R E G G A V Q N G S N H X S B G A S K G T
Q R E S A C B A R G A A G F A C T C G G A A G C K U C C G C G S E S I A E T C A M A R A D C E S R T C G G D S C C G C G T C G A M Q F T G A C C G C G G G G T F U G G Q A A S A S T / T C T G T A
C T G G T C T T C T T C T A G C S T T C C B C G C C C G C C G T G A T T T T G G S S T T C G C G G G C G C A C T T C T G A C T C O S C C C C C C C A C C C C G T T T C A C G G A T A

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2019-2020
2020-2021
2021-2022
2022-2023

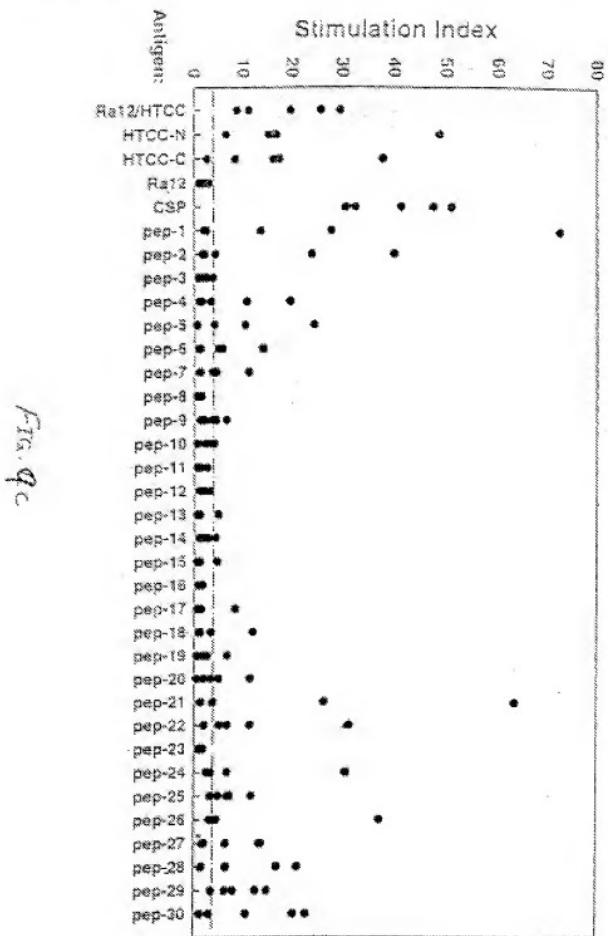
CGAAACGTCCTCTAAACGGGCAATT
→ 1226

GETTING A HEAD START

www.hTCG1.com

FIG. 9.

T Cell Epitope Mapping of HTCC-1



F_{TR}, q_c

Friday, July 23, 1999 8:45 AM
2000-07-23 TAU2-NDC-NPG (1 x 128) 24 1 Saturation

23

K G T F I K K V S E G A N A S T E D A G B A P Y C A B A G S
 CCACAAAGGTCGTGGTACGAAACGCTCTCTAAGGGCGATTC
 CGTTTTCCACUCCATGCTTGTGACGAAUUCGCGUAG
 ATGCTT [Biotin]

Fig. 9.

Monday, July 26, 1999 3:25 PM
Hg(164-302)-145-205(=139).mod (1 > 23) 51 c Sequences
5 sequences : 3 of 315 enzymes (Filtered)

FIG. 10

FIG. 10

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Wednesday, July 26, 1995 2:48 PM
801-3430-242-Ref ID: 39221-mod (1 > 3) 11:48:00 26/07/95

32

FIG. II

Monday July 26, 1982 2:42 PM
MFL 148, HORN 151-152, COT 11-12, S. 1-2 and 3 continuous

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FIG. 11

FIG. 12

Monday, July 25, 1999 2:43 PM
8734-021-HD-011-200; and 011-244-18867-Tennessee

FIG. 12.

FIG. 12

13

Figure 1: Nucleotide sequence of MTb59

cacgactgcccactgaaccctgaaacctgtcagcacaaaaccgtaaaggtaggaagacgaaaaagctatggc
 tgagttgcacalcccccgtgtatgcacattccagagcgcaatogaagagtacgttaaqgtcttttcacccgc
 ccacaccactgagagagaaagtccgttccgtcgatgcggggacggcaccggcacacgtcgaggg
 ttgcgcacatcggtgtatgcaccaaaagactgtcgatcccgccggggaaatccctcggtcgccgtcgccccccaa
 ccccgacgacgacacaycgtccggcgggtgtatccctcggtgacttcogatacatcgaaaggatcagca
 ggtcaagcgccacccggcgaaatgtttatcggttccgttggcgacgggtttttgggggggggtggttaa
 ccggatcgcccaacccgtatcgacggggcgccggagacgtcgactccgtatcccgccggcgccggagcc
 ccaggcgccctcggtgggtgcacccggcaaggcggtcgccagggagccgttgcagacccgggatcaaggcgat
 tgcacgcgtatgcaccccgatccggccggggccggccggccggccggatcccggt
 aacccggccgtctggcgatccacccatcccaaccatcgccagaacttggggatccgggtgatccaaagaa
 gcaaggccgtcggtgtatcggtggccatcggtggccagaaggaaactaccatcgccggggatccggccac
 actggaaaggggccgggtggatggactacaccacatcggtggggccggggatccgggttgcggccgg
 ttccaaatgggttgcgcgtatccacccgggttgcgcgtatccggccaaacttggatgtacggggggcaagca
 tgcgtcgatcatcttgcacccatcgatccatcgccggccggatcccggtatccgttgcgt
 ggcggccgtccggccggccgggtggccatcccgccgtatgttttgcgtatccatcgccggggatccggcc
 ggcgtccggccaaacttgcgtccggccatcccgccggatcccggttgcgtatccgggttgcgtatcccgagac
 caaggccaaacccgtatcccgccatcccgccggatcccggttgcgtatcccgccggatcccggttgcgtatcc
 cccggggatcccggttgcgtatccacccgggttgcgtccggccatcccggttgcgtatcccggttgcgtatcc
 agtccggggccggccggccggatccacccgggttgcgtatcccggttgcgtatcccggttgcgtatcccg
 gaaatcccgccggatccacccgggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc
 gttggagccggccggccgggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccg
 ggagccgttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccg
 cccggccgttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccg
 cccggacccaaacccgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc
 gaaatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc
 ggataaggctccggccaaaggaaaggccgttgaaaggccaaaggccggccggccggccggatcccggttgcgtatcc
 cccggccatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc
 caaggccccaggatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc
 ggcctacccatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcccggttgcgtatcc

14

Figure . : Amino acid sequence of MTb59

MAELTI PADDI QSAIE EYVSSFTADTSREEVGTVV DAGDGIAHVECLQGVMTQ2LLSPFGGILGV
LNLDENSVGAIVLGDFENIEECQQQVKRTGEVL5VPVGDFLGRVVNPLQQPIODGRGDVOSDTRRAL
ELQAPS VVIRQGVK EPLQTGIKAI DMTPIGRGQRQLIIGDRKTGKTAVCVDTILNQRQNWE SGD?
KKQVRCVYYAIGQKGTTIAAVRFTLEEGGAMDYTTIVAAAS2SAGFENLAPYTGSIAQHNMV EG
KHVLII PDDLT KQAEAVRAISLLRLRPPGREAYPGDVFYLNHGRLLERCAKLSDUGGSLTGLPI I
ETKANDISAYIPTNVI SITDGQCFL ETDLPNQCVRPAINVGVSVERVQGIAAGIKA MKEVAGSLRLD
LSQYRELEAFAAFASDILDAASKAOLERGARLVELLKQPQSQPMVVEQVVSIFLGTGGHLDSPVPE
DVRRFETELLOHMRASEEELTEIRD SQKLTERAADKLTEVIKNFKEG7AATGGGSVVVDENVEAL
DEDKLAKAEAVKVKKPAPKKKK

15

SECRET//NOFORN

16

Figure : Amino acid sequence of MTb82

MAKASETERSGPGTQPADAQTATSVRPLSTQAVFRPDFGQEDNFPHPTLCPTDTPQDRMATTGR
VRPPVRRLLGGGLVEIPRAPDIDPLEALMTNPVVVPESKRFCWCNCORPVGRBDSETKGASZGWC?YCG
SPYSFLPQLNPQGDIVAGQQEVKGCTAHCGLQWYIYLALORFVNNGRPVVLKGLVHSGDAEAEQAMAMAE
RQFLAEVVRHSITVQIFNNSVHETDRLHGDPUCYIVMSYVGGSLSKRSKGQKLPVAAEIAYLLSILPAL
SYLHSIGLVYNDLKPENIMLTSE2QLKLIDLGAVSRINSGFYLYGTGPGFQAPEIVRTGPTVATDIYT
VGRTLAALTLDLPTRNGRVVDGLPEDDPVLUKTVDYSGRLLRAIDPDPRORFTTAESMSAQLTGVL
REVVAQDTIGVPRPGLSTIFSPSRSTFGV DLLVAHTDVYLDGQVHAEKLTANEIVTALSVPVLDPTD
VAASVLUQATVLSQPVQTLDSLRAARMGALDADGVDFSESVELPLMEVRALLUDGDVAKTRKLDDL
AERVGWRWRLVWYRAVAELLTGQYDSATKHFTEVLDTFFGELAPKLAATAEELAGNTDEHKFYQT
VMSTNDGVTISAAGFLALARSAEGDRVCAVRTLDEVPPTSRHFTTARLTSAVTLLSGRSTSEVTEZQ
IRDAARRVEALPPTEPRLQIRALVLGQALDWLKDNCASTNHILGFPTSHGLRLGVEASLRSALAR
VAPTORHRYTLVDMANKVR9TSTF.

17

Figure 17: Amino Acid Sequence of secreted DPPD

DPPDPHQPDMDTKGTYC9GGRWGFQDLAVCDGEKYPDGSFWHQNMQTW7TG?QFYFDGVSGGEPLP
G999PQQCGGAIFSEQPNAY

SEQUENCE LISTING

Mtb43 (MTCC#2)

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:

 - LENGTH: 1441 base pairs
 - TYPE: nucleic acid
 - STRANDEDNESS: single
 - TOPOLOGY: linear

MOLECULE TYPE: cDNA

(XII) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTGTCG	GCATGGATT	TGGGGTTT	ACCTCGGAA	GTCAATTCAA	GGCGAATGTA	60
TTCGGTCCG	GGCGGGAGT	CGATGTAGC	GGCGGGGCC	GTCTGGGAGC	GTGGGCCCC	120
GGAGTTGACT	TGGCGGCGG	TCTGGTATGG	ATCGGTTGGT	TGAGGGCTGA	TGTTGAGCC	180
GTGGGGTGCG	CGGGGGGCGG	CGGGGGATGG	GGGGGGGGA	ACGGGGTATG	TGGGGTGGG	240
GGGGGGCACG	GGGGGGCTGG	CGAAGGGAGAC	GGCCACAGAC	GGGGGGGAG	GGGGGGAGC	300
GTTGGGGAGC	GCTGGGGCGA	TGGGGGGTGGG	ACATGGCTCC	GTGGGGGCGA	GGGGGGCGG	360
GTYGATGTCG	CTGGGGGGGG	GGGGCAATCTT	GGGGCAAAAC	AGTGCGGCGA	TGGGGGGCTAC	420
CGAGGGGGAG	ATATGGCGAAA	TGTGGGGCGA	AGAGGGTCCC	GTGAGGGTAA	GCTATAGGGG	480
GGCATCTGGG	GGGGGGGGGG	GGGGGGGGGG	GTTCGACTCGA	CCCGTGGCGAAG	GGGGGGGGCC	540
GGGGGGGGGG	GGGGGGGGCG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	600
TGCAACAAGG	ACATGGGGCC	AGCTGGGGGG	GGGGGATCTG	AGGGACATTCG	TGTCGCGGATT	660
GGGGGGGGAC	GCTGGGGCGC	GGGGGGGGGG	ATGGGGGGGG	ATGGGGGGGG	GGGGGGGGGG	720
GCAAGTCGGA	TGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	780
GGGGGGTCTAC	TGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	840
CAGACCCCTGG	ATTCGATCGA	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	900
TCCACTGAGT	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	960
GGGGGGTGGC	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1020
CTGGGACCGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1080
CAGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1140
GCGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1200
CAGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1260
GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1320
GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1380
GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	1440
GACGAGCTG	TCTGGGATTCT	GGGGGGCTAT	GGGGGGGATT	TTGGTGGCAA	CTTCAGGAAA	1441

(a) INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

MAIN MOLECULE TYPE: protein

[REDACTED] SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Asp Phe GLY Leu Leu Pro Pro Glu Val Asn Ser Arg Met Tyr
 1 5 10 15
 Ser GLY Pro GLY Pro GLU Ser Met Leu Ala Ala Ala Ala Ala Trp Asp

20	25	30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val		
18	40	45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala		
50	55	60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala		
68	70	75
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala		
85	90	95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala		
100	105	110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln		
115	120	125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp		
130	135	140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala		
145	150	155
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro		
165	170	175
Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly		
180	185	190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile		
195	200	205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr		
210	215	220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser		
225	230	235
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile		
245	250	255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile		
260	265	270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asp Ala Gly		
275	280	285
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu		
290	295	300
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala		
305	310	315
Gly Val Gln His Ala Ala Leu Val Gln Ala Leu Ser Val Pro His Ser		
325	330	335
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro		
340	345	350
Thr Phe Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met		
355	360	365
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg		
370	375	380
Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly		
385	390	395
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro		
405	410	415
Pro Pro Gly Asn Pro Pro Arg		
420		

Mtb40 (HTCC#1)

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCGATAG	CAGAGCCUTTC	ATCATCGATC	CAACGGATCAG	TGCCATTQAC	GGCTTGTACG	60
ACCTTCTGGG	GATTGGAAATA	CCCACCCAU	GGGGTATCCT	TTACTCTCA	CTAGAGTACT	120
TGAAAAAAAGC	CCTGGAGAG	CTGGCAGGAG	CGTTTCCGGG	TGATGGCTCG	TTAGGTTCCG	180
CCCGGGACAA	ATACGGCGGC	AAAACCGCA	ACACCGTGA	TTTTTCCAG	GAACCTGGAG	240
ACCTCGATCG	TCACTCTCATC	ACGCTGATCC	ACGACCAGGCG	CAACCGGTC	CAGACGACCC	300
GCGACATCCT	GGAGGGCGCC	AAGAAAGGTC	TGGAGTCTTG	GCTGTGGACK	360	
TGACTCTAC	CGGGTACCCC	TTATGGCCG	CTTTCAGAGC	CGGTTTTCG	420	
CGGGCGGGAT	GGCGTAGTG	TTGGCTACTT	GGTCGTGAA	ACGCTGTATCA	480	
ACGGCGACTCA	ACTCTCTCAA	TTGCTTGGCA	AAATGGCGGA	GTGGGTGGG	540	
CGGACATCAT	TTGGGGATG	GGGGACATCA	TCAAGGGCAC	CTCGGGAGAA	600	
TCATCACAAA	CGGGTGTCAAC	GGGCTGAAG	AGCTTGGGA	CAAGCTTCAG	660	
CGGGACTGTT	CTCTCGAGGU	TGGTGTGAAAC	TGGAGTCTTT	GGGTGGGCG	720	
TGACGGGGCG	GGACCAACCGC	TTTGGCGA	TTACTGGGTC	GGGGGTCTGT	780	
CGGCGATCTC	GGGCTTGCGT	CAAGCGGTA	GGCTGGGGAG	CTGAGCTAAC	840	
TGGCGGGCAT	TGGGGGCGGG	TCCGGTTTTC	GGGGCTTGGC	GAACCTGGGT	900	
CGGCGCTCAC	TCGGCGGGCG	GGACGGCGCC	GAGCTTATGG	CCGGTGGGCG	960	
AGCAGGTGCG	GGGGCACTGG	CAAGCTGGCT	GGGGCGAGGG	TTCCCAAGGT	1020	
CGGTAAAGCAT	GGGGGGCATG	CAACCGCTTT	GGGGGGGGTC	GAAGGGGACG	1080	
AGTACTCGGA	AGGGCGGGCG	GGGGGGACTG	AAGACCGCGA	ACGACGAGA	1140	
ACGGGGGGCG	TGGGCAAAAG	GGGGGGGTAC	GAACGCTG	GTGGAGACTG	1200	

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr	Kle Ser Ala Ile Asp Gly		
1	5	10	15
Lau Tyr Asp Leu Leu Gly Ile Gly Ile	Pro Asn Gln Gly Gly Ile Leu		
20	25	30	
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala	Leu Glu Glu Leu Ala Ala		
35	40	45	
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser	Ala Ala Asp Lys Tyr Ala		
50	55	60	
Gly Lys Asn Arg Asn His Val Asn Phe	Phe Gln Glu Leu Ala Asp Lau		
65	70	75	80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp	Gln Ala Asn Ala Val Gln		
85	90	95	
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys	Gly Leu Glu Phe Val		
100	105	110	

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 126 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Glu Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Glu Val His Ala Ala Ser Thr Arg Gin
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

Mtb9.9A (MTI-A)

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium tuberculosis*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGCTCTCTT TCAAGCTCAT AAGTTGGTG GGCCAGTCGG CGCGCGCTGCG ATATGGCAC
 60
 AATAACCGGT GTCCCATGGA TACCCGGACC GCACGACGGGT AGAGCGGATC AGCCGAGCGG
 120

GTGCGGARCA	CTACCGGGT	CACGGTCAGC	GCTGGCGCG	TCCGGAAAGAT	CGAGCCCCAGG	180
TTCCTCATGGT	CGTTAACGGG	TCACCAACRCT	CGACGGTGC	GCGCCCCCGC	GACCACCTGA	240
GCAACGCTCG	GCTCGGGCA	CGGGCGCGG	GCTGGCAACA	CCCCACGAT	GAGATGGGAG	300
CGGATCACCC	GTGCCATGAC	ATCAGCGGAC	GCTCGATATG	ACGGCCCGCC	GACACCGCCC	360
AGATCATCTC	TGAGCTCGGC	CAGCGGGCG	TCCGGCGGA	ACAGCGCCAG	CGGGCGTGAC	420
CGTGAGGCGA	CGATGCGCTG	CACCGACAGC	ACACCGCTGG	CGATCACCAA	CGGCTTGCGG	480
GTCGGCGAGT	CGGACNAACN	GTGAGATCTG	TTCAGGTCAC	CGAAATCGTC	GAGCGCTGGG	540
TCTTGGGGAT	CGAGAGCTC	CTGAAACATCG	AGGGCGCTGG	GCTGCTGGGC	ACACCGGCT	600
TCGGTCACGG	GCTTTCGTCG	ACCGAGGCCA	GCATCGAGTC	GGGGGGGCG	CGACAGGATGT	660
CAGCGTCCT	GGCGTTGACG	GTGGCGGAC	GTCAGCGAC	CGACTCTTC	AGAGAGCGT	720
TGCTGGGAT	AATTCGGAGA	GGAAACAGC	ATGTCGTTG	TGACACACA	GGGGGAGGCC	780
CTGGCAGCTG	CGCGGGGGA	CCTACAGGGT	ATTGGCACGA	CGATGAGGG	CGAGACCGG	840
GCCCGGGCTG	CTTCCAAACG	CGOACTAGG	CGGGCGCGG	CGGATGAAGT	ATCAGCGCTG	900
ACGGGGGCTC	AGTTTGCTG	GEACCGACG	ATGTCACCAA	CGTTCAGCGC	CGAGGGCGG	960
GGCTTACAG	AAATTTCTGT	GRACAGCGT	GTGGCCAGTT	CTGGCTCAT	CGCGGCCACC	1020
GAGGGGGCCA	ACGGAGCGCC	TGGCGGTC	ACGGGGCTGGC	CGGAACCTGC	TGAAAGGAGAG	1080
GGGGAAACATC	CGGAGTTCTC	GGGTGGGGG	TTGGCGGAGC	GGCCGAGCGA	TTCAGNTATC	1140
GGGCTCCATA	ACACGACAGC	ATCTAGGGC	TCACTACTAA	CGAGACAGGC	AAATGGGCCT	1200
CACTTTTAT	GACGGGATG	CATGGCGATC	GGGACATGGG	GGGCGUTTTT	GAGGTGACCG	1260
CCAGACAGGT	GGGAGGCGG	GCTGGCGGA	TGTTGGGCTG	GGGGCGAAAC	ATTCGGGTG	1320
GGGGCTGGAG	TGGCGATGGG	GRGGGGACT	CGCTAGACAC	CATGACCTAG	ATGAAATCAGG	1380
CUTTTGCGAA	CATGCGTGAAC	ATGTCGACG	GGGTGCGTGA	CGGGCTGGTT	CGCGACGCCA	1440
ACATACAGA	ACAGCGACAG	CAGGGCTCCG	ACGAGATCT	CGACAGTTG	CGCCGAAAGC	1500
CACAGCTG	TAACCTTCT	CACTTAAAGA	GAACACCAAT	ATGACGATTA	ATTACCACTT	1560
CGGGGACCTC	GAACGCTCATG	GGGGCGATG	CGGGCGCTGC	GGGGCGCTCG	TTCAGGCGGA	1620
GCATCAGGCC	ATGTTTGTG	ATGTTTGTG	CGGGGGGTGAC	TTTTGGGGCG	GGGGGGGTT	1680
GGTGGCTTGC	CAGGAGTTC	TTACCCAGTT	GGGGCGTAA	TTCCAGGTGA	TCTACCGGCA	1740
CG						1742

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGATTGCG	TTCCGGGGCG	GGCGGAAAGC	CAACAACTTC	GCTGGGGTGG	TGGCACACGG	60
GTTTGGCTGG	GTCAAGCTGG	CGAACTCCAA	TTATTTGGTG	CTCGTGTGGG	TTGCTGGGCT	120
CGAAATTACCC	CACCGGAAAG	ACGACATGGT	TTGGTTTCT	CGGTCACTGC	TACTTGGGGA	180
CGGGCATGGC	GGGGTTTCTT	ACCTCGATCC	CAACAGAGCT	GAACCTTCGG	CCAGGGGGCA	240
CAACGGCTGG	TCTGGGGCGA	GGCTGGTACG	CAACGGCCACA	ATTGCCCGGC	CTGGGTGACG	300
GCCCGGGCGT	GTGGCGGAGT	TTGGGGGGGG	CGGAGCGCGT	CGGGGAGTTG	TGGGTGCCCC	360
CAAGTGGGCC	CUTGGCGGCT	CGGGCGCTTG	GGAGGAGAGC	TGAGGGCGGC	ACGCGGATGT	420
CGCTCATCGG	CGAGAGCGGT	AGCTGGCGTC	AGGGAGGCGT	CGTCTGGGAC	ATACCGCTGG	480
CGAGAGCGGT	GGGGCGTACA	GGGGCGCTTG	CTCACCGATA	CGGGTTCCCG	CGACGCTGAA	540
TTACCGGGCG	TGCGTGGGG	GGTAGAGCTT	CGATCGGTC	TGGGGGGCGG	CGGAAANTGC	600
TGCGAGTACG	GATCGGCGGC	GGCGCGTGT	AAACGGCCGA	CACGGCACTA	TCAATGCGCA	660
CGGGGGGGGT	TGATGCCAA	TTGAGCGTCC	CGACGGGGGT	TTATCTGGG	CAAGATTTCA	720
TOCCGAGGCC	GGTCGGTGG	CGGATAATAA	CGCTGGTCAG	CGGGACTCTT	CGGGCTGAAAT	780

TGCGTGTCT	GGGGCCCCGC	TGACCGGGA	GTCATCTGAG	TGGGCCCAA	ACCCGGTCAA	840
ACGGCTTATC	TGTGGGTTTA	CCACAGGTTA	ATTTCGGGTTG	CAACTGGTGT	ACACTCTCG	900
AACGGGGTGC	ATCGAAATCA	ACTTCTTCCG	TTCGATGTTG	CTACTCTCT	GGAGAACAGC	960
GTTGCTGGG	TIAARTGGGA	GAGGAGGACA	GTATGGTCTT	CUTGACCEACA	CAGCCGGAAAC	1020
CCCTGGCAGC	TGGCGGCGGC	AACCTACAGG	GTATGGCAC	GACAGATGAAAC	GCCCAGAACG	1080
CGGCCCGCGU	TGCTCCACCC	ACCGGGATAG	TGGCCGAGG	GGCGGATAGA	GTATCGGCG	1140
TGAGGCGGCG	TCACTTGGCT	GGCGACGGCG	AGATGGACCA	ACACGGTACG	GGCCAGGCG	1200
CGCGACATTC	CGAATATTC	CTGAAACACRC	TGTGGGCGAG	TCTGGGCTCA	TACGGGCGCA	1260
CGGAAGGCGC	CAACGGCAGCC	GTGCGGCGGT	GTGCGGCGT	CGACGAACTT	GTGCGGAGG	1320
AGGGGGGARCA	TGGCGATGTC	TGGGGCTGAG	GOTGGCGCCA	GGGCCCGGCA	GATTCAAGCTA	1380
TGGCGCTCCA	TAACAGCAGC	CGATCTAAGG	ATTCACTACT	AGGGAGACAG	GCACATGGC	1440
CTCACGTTT	ATGAGGGATC	CGCATGGCTAT	GGGGGGATAG	TGGGGCTT	TGAGGTTTCA	1500
CGCCGAGAGC	GTGGGAGGAC	AGGTCTGGGG	GTATGGGGG	TGGCCCGAAA	ACATTCGGG	1560
TGGGGCTCT	ATGGCGATCG	CGCGAGGCGAC	CTCGCTAGAC	ACCATGAGCT	ATATGAACTA	1620
GGGGTTTCG	AACATCTGTA	ACATCTCTCA	CGGGGGTGGT	GTGGGGGGGT	TTGGCGACCG	1680
CAACAACTC	GAACAGCTG	AGCGGGCTTC	CGCAGAGATC	CTSGAGCAGT	AGCCCCGAAA	1740
GGCACACCTG	CTACAGCTTT	CTACRACATAG	GAGAACACCA	ATATGACGAT	TAATTACCG	1800
TTCGGGGACU	TGCGACGCTA	TGGGGCCAGG	ATCGCGGCTC	AGGGCGCTC	GCTTGGGGG	1860
GAGCATCAAG	CGATCTGGCT	TGATGTGTTG	GGGGGGGGTG	ATTTTGGGG	GGGGGGGGGT	1920
TGGGGCTT	CGGCGAGGTT	CATTACCGAG	TGGGGCGCTA	ACTTCCAGGT	GATOTACGAG	1980
GAGGCCAACG	CCACCGGCA	GAAGGTGAG	GTGGGGCGGA	ACAAACATGCG	GCACAAAGCG	2040
AGCGGCGTGC	TGGCGAAGCTG	GGCTCTAAAC	TGAACTTCTAG	TGGCGGCGAC	ACRACCAACCA	2100
GGGGCTTGTG	TGGGTGTTGC	TGAGCTTAAAC	TAGQACTCGA	CGCTGAGGT	AGGGATGGAT	2160
CAACAGAGTA	CGCGCACCGT	CATCGACGTC	AACTGGTACGG	GTTTGGGGAT	GTTTCACTCG	2220
CTACTGGATA	TGGCGACGCT	TGCGCTTGAQ	TGATCTTGCG	GGCGCTACGT	ACACCGGAT	2280
TCTAACATGCT	GGCTTAAAGCA	GGACCGGGGG	ATGCGGGTCA	TGCGCGAGGA	GGGCATTGTC	2340
CTCAACAGACG	CGGTCAACGA	ACAGGTCGGC	GGCGGGTGA	AGCTTGCTTC	CGACCTGTAT	2400
CTTGGAACTG	TGGGGCTGT	GTCACTGGG	AGTCTCTGT	ACGGGTCAT	AGGACGAGAG	2460
AAACGATGTC	CGGGTGGCGG	TGACATCTCT	GAACATGAGT	TCCGGGTGT	TTGGGGGGG	2520
CGAGGCCAGC	ACTGGGTGTC	GGGGGGTAGG	GTGGGCAATG	ACATCATGGT	CGTGGAGTC	2580
AGCGGCTCGC	ATAGGGCGCTC	GATGCCCGCA	CTGTTAATGG	AGGCTCTGGG	TGGGATTTAC	2640
CACCCGGACG	CAGCGGGATG	CAACGGCTTC	RAATGTGCAA	TGGAGGAGAT	CTCGTGGCGGA	2700
ATTGGGGACG	AGCGCACAGG	CGTGTGCGT	GGCGACCGGA	TGGATACGGA	TCATGGACCG	2760
GGCGGGATAC	TGGCGATCT	CGTTGAGCAC	GACCCGGGUCC	CGGGGGAGG	TCTGGCGACAT	2820
CGATGGGGTC	TTGGCG					2880

(2) INFORMATION FOR SEQ ID NO:29:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(x) ORIGINATOR SOURCE:

- (ii) ORGANISM: *Mycobacterium tuberculosis*

4413 SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Thr Ile Asn Tyr Glu Phe Gly Asp Val Asp Ala His Gly Ala Met
          5                   10                  15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Cys Ala Ile Ile
          20                  25                  30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
          35                  40                  45

```

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 85 90

Mtb9.9A (MTI-A) ORF peptides

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala		
1	5	10
		15

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln		
1	5	10
		15

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gin Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gin Glu Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Phe Ile Thr Gla Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15
Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gin Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Tyr Gla Gln Ala Asn Ala His Gly Gln Lys Val Gin Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala
1				5					10					15	

Mtb9.8 (MSL)

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGATTCCGA	TAGCGGTTTC	GGGCCCTCGA	CGGGCGGACCA	GGGGGGCGAG	GGCTCCGGAAC	60
GGGGGGGCGG	GACGCTGGGA	TTGGCGGGGA	CGCGAACCCMA	AGAACCGGCG	GTGGCGGGCGG	120
TGGGUGCTGC	CUCACTGGCC	GGTGATGAGT	TGCGCGAACGG	CCCCCGGATG	COSATGGTGC	180
CGGGGACTCG	GGGAGGAGGC	ASCAACGGAC	CGGAGGGCGCC	CGACGGGATG	CGGAGGAGGG	240
GAGGGACACG	CTTACCGCAC	GACAGCAAGT	AACGGAATTG	CGAATCAGGT	GGACCCGGTAC	300
GUGTCGAG	GAGAGATGTT	ATGAGCTCTA	TATGCCACAG	TIGGTGGCTT		360
CCACAGTCGG	CTTTCGCGGC	AAAGCGCGGC	TGATGCGCGA	CACGATCGGT	CAGGCGCGAC	420
AGGGCGGCAT	GTGCGCTCA	GGCTTTCAAC	AGGGGGGAGTC	GTGGCGCGCG	TTTCAOGCGG	480
CCCATCGCCC	GTTCGCGCG	GGCGCGCGCA	AAGTCACAC	CTTGTTGGAT	GTGCGCGAG	540
CGAATCGGGS	TGAGCGCGGC	GGTACCTATG	TGGCGCGCGA	TGCTG		585

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Leu	Leu	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser
1							5			10				15	
Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala
							20			25				30	
Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser

35	40	45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys		
50	55	60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala		
65	70	75
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly		
85	90	95
Phe		

Mtb9.8 ORF peptides

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met			
1	5	10	15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val	Ala	Gln	Ala	Asn	Lys	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	Ala	Ala
1				5				10					15		
Asp Ala															

Mtb39A (TbH9)

(2) INFORMATION FOR SEQ ID NO:106:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTQCGAAGTTGC	TGGGGCCGTT	TGAGGATGGA	GTGACAGCTGT	CTTTCGTGAT	60
GGCATTCGAA	GGAGATGGTG	CGGGUGCGCG	TGACACCTTG	CAGAGCATCG	GTGCTTACAC	120
TGTGGCTAAC	AATGCCGCTG	CGGCGGCCCG	GGACGACTGG	GTGGTTCGCC	CGCTGCGCGA	180
TGAGOTGTGG	GGCGCTGACTG	CGGGCGATCT	CGCGCGATGT	ATCGATGTCCT	240	
GACGCTCGG	GTCTGCTCGA	TTCATGACCA	GTGTTGTC	ACCGTTGCGA	GAAGCGCCAG	300
CTCGTATGCC	GGCGACTGAG	TCGCAATCG	GGCGCGCG	AGCTAAGCCA	GGAAACRGTGG	360
GGACGAGAAA	CCACCGAGAAA	TAAGGACGAC	TAATGTTGGA	TTTGGGGGCG	TTTACGACCG	420
AGATCGAACG	CGACGAGGRT	TACGGCGCG	CGGGTTCGCG	CTGGCTGGTG	GCAGCGCGTC	480
AJATGTTGAA	CGACGAGGCG	AGTGGACCTG	TTTCGCGCGC	GTGGCGCTTT	CACTCGTGG	540
TCTGGGGTGT	GACCGTGGCG	TCTCTGGATG	GGCTGCTCG	GGGTCTGATG	GTGGCGCGCG	600
CCTCGCCGTA	TGTCTGCTTG	ATGAGCTCGA	CGCGCGCGCA	GGCGCGCGTC	ACCGCGCCCG	660
AGCTCGGGGT	TGCTCGCGCG	GGCTACCGAGA	CGCGCTATGG	GCTGACGGTG	CCCCCGCGCG	720
TGATCGCGGA	GAACCGTCT	GAACGATGGA	TCTGTATGTC	GACCAACCTG	TTGGGGCGAA	780
ACACCGGCGG	GATCGCGGCG	AACGACGCG	AATACCGCGA	GAATGCGGCC	GAAGCGCGCG	840
CGCGATGTT	TGGCTACCGC	GGCGCGCGCG	CGACGCGCGC	GGCGACGTTG	CTGCCUTTCG	900
AGGAGGCGCC	GGAGATGACC	AGCGCGCGGT	GGCTCTCG	GCAGCGCCCG	GCAGCGCGCG	960
AGGCGCTCGA	CAACCGCCCG	GGCGACCGAT	TGATGACCA	TGTCGCCCCG	GGCGTGCAC	1020
AGCTCGCGCA	GGCGCGCGCG	GGCACACCG	CTTCTTCMCA	GCTGGGTGCG	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGTGTG	CGGATGACG	ACATGTTGTC	GATGCCAAC	AACACATGT	1140
CGATGACCAA	CTGGCGTGTG	TGATGACG	ACACGATGCG	CTCGATGTTG	AAGGGCTTTG	1200
CTCGGGGGCG	GGCGCGCGCG	GGCTCGCGAA	CGCGCGCGCA	AAACCGGGTC	GGGGCGATGA	1260
CTCTCGCTGGG	GGGCTCGCTG	GGTCTCTCG	GTCTGGCGCG	TGGGGTGGCG	GCACACTTGG	1320
GTGCGGGGGC	CTGGGTGCGT	TGTTTGTG	TGCGCGACGG	CTGGGGCGCG	GCACACCGAG	1380
CACTCACCCC	GGGGGGCGCG	GGGCTCGCGG	TGACCGCGT	GACCGCGCG	GGGGAAAGAG	1440
GGCCCGGGCG	GTGCTGCGG	GGGCTGCGG	TGGGGCGAGT	GGCGCGCGAG	GGCGGTGCG	1500
GGCTCAGTGG	TGTGCTGCGT	GTGCTGCGG	GACCTATGT	GATCCCGCGAT	TCTCCGGCGG	1560
CCGGCTAGGA	GGGGGGCGCG	AGACTGTGTT	TATTGACCA	GTGATCGGGG	GTCTCGGTGTT	1620
TTCCGGGGCC	GGCTATGACA	ACAGTCATG	TGCTATGACA	GTTCAGGTTA	TTAGGGTCCAG	1680
GTTCACACAG	GAAGACGGCA	ACATGCGTC	ACGTTTTATG	ACGGATCCCG	ACGCGATCG	1740
GGACATCGCG	GGCGCTTGG	AGGTGCGACG	CCGACGGTG	GAGGACGAGG	CTCGCGCGAT	1800
GTGGGCTCCC	GGCCAAAACA	TTTCGGGTGC	GGCTGCGAGT	GGCATGCGCC	AGGGCGACCTC	1860
GCTAGACACC	ATGGCGACGAG	GTTCGCGAC	ATCTGAAACA	TCTCTGACGG		1920
GGTGCCTGAC	GGGCTGCGTC	GGCGCGCGCA	CAACTACAGG	CAGCAGACG	AGGGCGCCCA	1980
GCAGATCTCC	AGCGNGCTAC	GTCACTCGCT	GGCGACAAAT	ACCTTTTACAA	GGCGAAAGAGA	2040
ACAGGTTGGA	TGACCTCGCA	CTATCGATTC	GGGATGTTGCG	ACGCTCACCG	CCCCATGATC	2100
GGCGCTCAGG	CCGGGTGCG	GTAGCGACG	CATCGACCGA	TCAATTGTTGA	TGTGTTGAC	2160
GGGAGTGA	TTTGGGGCGG	GGCGGTTGCG	GGCGCTGCG	AGGGGTTGCG	TACCGAGTTG	2220

GCCGCTAACT	TCCAGGTGAT	CTACCGAGCAG	GCCPACGCC	ACGGGCAGAA	GOTGCAGGCT	2280
GCCCCCAACA	ACATGGCGA	AACCGACAGC	GCCGTCGGCT	CCAGCTGGGC	CTGACACCAAG	2340
GCCAGGCCA	GGGACCTGGT	GTACGGCTGG	AUTTCCCTCG	GTGATCCTTC	GGGTGGCACT	2400
CTAAGTGTCTC	ACTGTGGGCG	TGTGGTGTG	TTCGCTGTTG	GGGGTCTCTT	CCTGCTGTGT	2460
CAGTGTCTCT	GGGCGCTGGG	CTAGGACCTTC	GAGGCCAGG	TAGCGCCGTC	CTTCGATCCA	2520
TTCGTCGGGT	TGTTCGGCGA	GGACGCGCTTC	GACGAGGCGG	ATGATCGAGG	CGCGGTGCGG	2580
GAAGATGCC	ACGACGCTGG	TTGCGGCGTCG	TACCTCTCGG	TTGAGCGCTT	CCTGGGGGTT	2640
GTTGGACCGA	ATTGGCGCC	ADATCTGCTT	GGGGAAAGCG	GTGAAACGCCA	GCAGGTCGCT	2700
GCGGCGGCT	TGGAGGTGCT	GGGCCACCCCG	GGGAGGTTTG	TGGTCAAGAC	CTTCAGTAC	2760
CGGATCATAT	TGGGCAACAA	CTGATTCCGG	GTGGGCTGCG	TGTAGATGCG	ACTGCCAGCG	2820
GTTGGCGACC	CACCGCGAGG	AGGGCTTCGG	GTGGGCTGCG	ATCAGAITGG	CTGGCTAGEG	2880
GTTCTGCCAG	CGCTGCCAGG	CCGTCGGGGG	CAGGGTGGCG	CCGATCGCGG	CCACCCAGGCC	2940
GGGTTGGCGG	TGCGTGGTGA	CCAGCGCGAC	CCGGGACRNG	CCGGGGCGGA	CCAGGTCGCG	3000
GAAGAACCCC	AGGCCAGGCCG	GGGGCTCTTC	GGGGGAGGTTG	ACCTGGATGC	CCAGGAGTC	3068

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
i						5					10				15
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp
								20					35		30
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
						35					40			45	
Val	Val	Trp	Gly	Ley	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
						50					55			60	
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr
65								70			75			80	
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	
						85				90			95		
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala
						100				105			110		
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Gly	
						115				120			125		
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met
						130				135			140		
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Thr	Ala	
145							145				150		155		160
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Ala	Pro	Glu	Met	Thr	
						165				170			175		

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

Mtb32A (TbRa35)

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATACGGTG GTGTAGAGAAA ATGCTCCCGC CCGGACCCCTT AAGGCTGGGA CAATTCTGAA

60

TGCTGACCCCC	GACACAGGAG	GTTACGGGT	GAAUCAATTG	CGGCGCCGCT	CACTCNGGTG	120
GTCATGGTT	CTGAGCGTGC	TGGCTGCCGT	CGGGGGTGGC	CTGGCCACG	C CGCGGCCCCA	180
GGCGGCCCCG	CGGGGGCTTG	CGCAGGACTG	GTTCGGCGAC	TGGCCCGCTG	TGGCCCTCGA	240
CCCCTGCGG	ATGGTCCCG	AATGGCGGCC	ACAGGGTGGC	ACATCAAC	CCAAACTGGG	300
CTACACACAC	GGCGTGGGG	CGGGGACCCG	CATGTCATC	GATGCCAACG	GTTCCTGTCT	360
GACCRACAC	GAAGTGTACG	CGGGGGCCAC	CGACATCATC	GGGTTTACG	TGGCGCTCCG	420
CCAAACCTAC	GGGCTGATG	TGGTGGCGTA	TGGCGCAC	GGGGTGGCG	GGGGTGGCG	480
GTCGGCGCTG	GCGGTTGGGC	TGGCTGGCG	GGCGATCGT	GGGGGGCTCG	GGGGTGTGTA	540
GCGGGTCGTC	GGGATGGGCA	ACAGGGTGGG	CGGAGGGGUA	ACGGGGCGTG	GGGGTGGCTGG	600
CAGGGTGTGTC	GGCGCTGGCC	AAAGCGTGG	GGGGTGGGG	GGGGGGGGAA	GGGGGGCTGG	660
GACATGAAAC	GGGGTGTGTC	AGTTCGATC	CGGCGTGGGG	TGGCTGACGG	GTGGCGAAAGA	720
CGTCGTCACG	GGCCTAGGAC	AGGTGTCGG	TATGGACAC	GGGGGGTCG	ATAACTTCCA	780
GCTGTCGGCG	GTTGGGGCAGG	GATTCGGCAT	TGGCGATGG	GGATCCCGG	GGATCCCGG	840
CCAAATCGGA	TCTGGTGGGG	GGTCACCCRC	CGTCATCAC	GGGGCTTACG	CTTCCTCGG	900
CTTGGGTGTT	GTGGACAAAC	ACGGCAACCG	CGGACGAGTC	GAACCGCTGG	TGGGAAAGCG	960
TCCGGGGCGCA	AGTCTGGGCA	TTCGACCGGG	CGACGTGATC	ACCCUGGTCG	AGGGCGCTCC	1020
GATCCTACTG	GGCACCGGGA	TGGCGAAGCG	GGTAAACGGG	CATGTCATCG	GGGAGCTCAT	1080
CTTCGGTGTAC	TGGCAAAACCA	AGTGGGGCGG	CGGGGGTACA	GGGAACCTGA	CATTGGCGA	1140
GGGACCCCCG	GGCTGATTTG	TGGCGGATAC	CACCGGGCGG	GGGGCACTTT	GGATTGGCGC	1200
CAGGGCTGTAT	TGGGGGGGTA	GGCGGGGAGT	TGGCGTGTGG	GGGGGGCTGG	CATTGGTGGAA	1260
GGAAATGAAAC	AGGCGAACAA	CGGGTGGG	CGACCTTCGGG	TGGAGGGGAG	TTACGTGAAA	1320
GGGGGGTGTGG	TGGAGGATCC	GGATGGCGGA	GACTGGGGGA	GGGGGGGGGG	GGGGGGGGCC	1380
GAACGGGACCT	GGTTTAAAGC	CGGGGGCTTG	TAGGGGGGG	TGGTGGGGG	GTTCCTGGAC	1440
GGGAGCGGGG	AGGGTTCGGH	GGGATGGG	GGGACTCATG	ATGGCGCTGA	CTTACCTCG	1500
TGGCTGGGG	TGGACTGAT	CTGGTGGCGC	GGTTCCTGAG	ATCACCGCT	GGGGGAGGGC	1560
GGTTACCGACA	TGGCGGACTG	CTACAGGTO	CTGGGGGAAT	TGGCGGAGGT	GGGGGAGGGC	1620
GTGGGGCTGG	TGGACACCGG	TGACCGGGGA	GGTATGGCGA	ATCATACCGA	CTGGGGTATG	1680
ATGACACCT	GGGAGTCCGA	GGGGTGGGTT	CAGGAGTCCC	GGGGGGGACCC	AGACGGGACG	1740
TACGGTGTACT	ATTACGGTGTG	GAGGGACACC	AGGGAGGCGT	ACACCGAGGC	CGGGATCATG	1800
TTGGTCGACA	CGGAGGAGTC	GAAGTGTCA	TGGCAACCTG	TGGGGCGACA	GGTTCCTACTG	1860
GGACCGATTC						1920

(2) INFORMATION FOR SSO ID NO: 79:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

115	120	125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly		
130	135	140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly		
145	150	155
Gly Glu Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu		160
165	170	175
Gly Glu Thr Val Val Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr		
180	185	190
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser		
195	200	205
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr		
210	215	220
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe Ala		
225	230	235
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly		240
245	250	255
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu		
260	265	270
Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val		
275	280	285
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile		
290	295	300
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp		
305	310	315
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln		320
325	330	335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly		
340	345	350
Pro Pro Ala		
355		

M168.4 (DPV)

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGTGGCAAGG TCGTTGACCG CGCGGGGCGCG GGTGCGCTCG GCAGATCCCG TGAGACCGCGT	60
CATTAAACACC ACCTGCAATT ACUGGGCAGGT AGTAGCTTCG CTCRACCGGA CGGATCCGGG	120
GGCTGGCGCA CAGTTCAAGG CCTCACCGGT GGCGCAGTCGC TATTTCGCCA ATTTCCTCCG	180
CACAGCGGCC CCTCAAGCGG CTGCGCATGCG CGCGCAATTG CAAGCTGTGCG CGGGGCCGCG	240
ACAGTACATCC CGCGCTTGCG AGTCGCTTGC CGCGTCTCTGC AACAGTACTATT AAGCCCCATGC	300
GGGGCCCATC CGCGGACCGG GCGTCGTCG CGGGGCTAGG CCAGATTGCC CGCGCTCTCA	360
ACGGGGCGCA TCCCGGAGCC CGCGCATGTC CGCGGGGCTA CGCGAGATG CGCGGCTCT	420
CAACGGGGCG CATCTCGTG CGAATTCCTG CAGCCCCGGGG GATCCACTAG TTCTAGAGCG	480
GGCGGCCACCG CGGTGGGAGCT	500

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1					5					10				15	
Val	Asp	Ala	Val	Ile	Asn	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	
					20				25					30	
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
					35				40			45			
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro
					50				55			60			
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
											65	70	75	80	
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Aan	Aan	Tyr
						85				90			95		

Mtb11 (Tb38-1)

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA	GACCGATGCC	GCTTACCCCTTG	CCTCAGGACGGC	AGGTAAATTTC	GAGGGATCT	60
CCGGCCGACCT	AAAANCCCGC	ATGGACGAGG	TGGAGTCCTTG	GGCAGGTTTG	TTCGAGGGCC	120
AGTGGCGCGG	CCGGCGGGGG	AAGCCGCCCC	AGGCCCGCGGT	GGTCGCTTC	CAAAAGACAG	180
CCAAATAGCA	GAAGCAGGAA	CTGGACGAGA	TCTCACCGAA	TATTCGTCAG	CCCGCCCTCC	240
AATACTGG	GGCCGACGAG	GAGCCGAGC	AGGCCGCTGTC	CTCGCAAATG	GGCTTCTGAC	300
CGCTTAATAC	GGAAAAGAAC	GGAGCA				327

(2) INFORMATION FOR SEQ ID NO:88:

- (1) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly

20	25	30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala		
35	40	45
Ala Val Val Arg Phe Gln Ala Ala Asn Lys Gln Lys Gln Glu Leu		
50	55	60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg		
65	70	75
Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe		
85	90	95

TbRa3

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGGAGAGTGTG TGCACATCG CGGGACCAGC CCCACATCCG CCGAACAGGC	60
GGCGCGGGAG CGCGTCGAGC CGGCCCGGGA TAGCGTCGAT GACATCGCG TGCGTCGGGT	120
CATGGACAG GACATGGCCG TGGACAGCGC CGGCAGAGTC ACGTACCGCA TCAAGCTCGA	180
AGTGTCTGTC AAGATGAGC CGCGGAAACG GCCTAGCAC GGGCCGGGGA GCGAGACGCA	240
AAATCGCGG GTTGGCGGT GATGGTGCG ATTTCGTTTC TGCTCGCGKA GCGCTACCGA	300
GCGCGGCCCA GCTCGCGTGT CTGGCGTATCA CGGGCGTCA CGCGGATTCG GCGGCCGACG	360
CGGGGAGTTAA TGCTTCGCGT CAACCGAACG TGCGCGATTCG GCGGGGGAGC TGTATCGATGA	420
CGCTTGCCAG CGCTTCGATG CGGAGATTCG CGAGGAAAC GTGCTGCCAG GCGGGTAAGGA	480
AGCGTCCGTA GCGGGCGGTG CTGACCGGCT CTGCGTCGCGC CCTCACTGCG GCGAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Try Glu Gln Ala Ala			
i	5	10	15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val			
20	25	30	
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile			
35	40	45	
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln			
50	55	60	
Pro Arg			
65			

38kD

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1993 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGCGCGGGTG CTGGAGGAAG GGCCCACCGA ACAGCTGTTC	TCTTGGCCGA	40
ACCATCGGGA AACCCCGGA TACCTGGCG GACTGTCGGG CGACGTCAGG	GACCGCAAGC	120
CGCGAAATTG AAAGCTATGG CGTGAATAATT CGTTTGCTATA CGCTGTGGC	180	
CGTGTGACCG GTGCGGCCGC TGCTGTCTAG AGCGCGGGGC TGTCGGCTGA	AACCAACGAG	240
CGTTGGCTCT GAACCGGGCGG CGCGCGCGG TACTGTCGGG ACTACCCCGG	CGTGTGCCCC	300
GTGAGCGTTT CGGGGACGGG GTAGACGCTG GCTTCTACCGG CTGTTCGACCC	TGTGGGGTCC	360
GGCCCTTTCAC GAGAGGTATTC CGAACCTTCAC GATCCACCGT CGGGCACCG	GTTCGTGGTC	420
CGGGATCCCG CAGGGCGGCC CGGGGACGGT CAACATTTGGG GCCTCCGACCG	GTATCTGTC	480
GGAGGTGAT ATGGCGGCCG ACAGGGGGT GTGAAACRCG CGCTTAGGCCA	TCTCCGCTCA	540
CGAGCTCAAC TACAACCTGC CGGGAGTGAC CGAGCACCTC AAGCTGAACG	GAAAATTCCT	600
GGCGGGCATG TACCAAGGGCA CGATCAAACG CTGGAGACAC CGCGAGATCG	CTGGCGCTCAA	660
CCCCGGGGTG AACCTGGCGG GCACCGGGGT AGTTGGCTG CACCGCTCCGG	ACGGGTCGGG	720
TGACACCTTC TTGTTCTACCG AGTACCTCTGC CRAGCAAGAT CCCTGGGGCT	GGGGCAAGTC	780
GGCGGGCTTC CGACCCACCG CGAGCTTCCC GGCGCTGGCGG GTGGGGCTGG	GTGAGAACCG	840
CAACGGGGGC ATGGCTGACCG GTGGCGGCCG GACRACCGCGC TCGTGGGCTT	ATATCGGCAT	900
CAAGCTTCTC GACCCACCGA CTGCAAGGGG AGTCCGGCGAG CGCCACACTAG	CGAATGCTC	960
TGGCAATTTC TTGTTCTCGG AGCGCCAAAG CATTCAGGGG CGCGCGGGCTG	GTTCGGCATC	1020
GAACACCCACG CGGCGGGGGG CGATCGAGCG CGCGGGGGGG AGGGCTACCC	1080	
GATCATCAAC TACGAGTAGCG CGATGTCGA CRACCGCCAA AAGAGCGCCG	CCACCGGGCA	1140
GACCTTGCACG GCAATTCTCGC ACTGGGGCGAT CACCGCGCGC AAGAAAGGCTT	CGTTCTCTGA	1200
CCAGGTTCACT TCCGAGCCCG CGGCGGGGGG GTGTCGGTGAAG TTGTCGTGACG	CUTTGATCGC	1260
GAAGATTTCC AGCTTACCGT GTGACCCACCG AGCGCGACAGC AACCTCCGTC	GGGGCGATGG	1320
CGTCCTTTCG GGAGCATCTG CGCGCGGGTGC GGTCGAAGTCG CGCGCGCTGG	CGCGGGCATCG	1380
CGGGGGTGGG GTGGGGATAG CGGGGGCTTG CGCGCTCTTG CGCTGGCTTT	CGTGTGGTG	1440
GTGCTGGTTC CGGGGGGAT CGGGGGCTTC AGGGCTAACG CGTTCGATT	CTTCACCGGC	1500
ACCGAAATGGA ATCCAGGCGA CACCTACCGG GAAACCGCTG TCACCGACCG	GTGGCCCATC	1560
CGGTGGGGCG CTACGACCGG CGGTGGCGGC TGATCGCTGG GACGCTGGCG	ACCTCGGGAA	1620
TGCGGCTTGG CCGGGCTCTGC CGGGGGCTTG TAGGAGCGCG CGCTGGTGATC	GTGGACCGC	1680
TGCGGAACCG GTTGGCGGAG CGTGTGGGAA TATGCTGGAA ATGGCTGGCG	GGAATCCCGCA	1740
GCGTGGTGTG CGGGTTGGG CGGGGCGATGA CGTTCGGGGCG GTTCATCGCT	CATCRACATG	1800
CTCCGGGTGAT CGGCTCACAC GTCGGCGATG TGCGGGTGTG CTGACTTGG	CGGGCGACCC	1860
CGGGCAACGG CGGAGGGCGAT TTGGTGTGCC GTCTGGGTGTG GGGGGTGTGATG	GTGGTTCCCCA	1920
TTATGGCCAC CACCACTCAT GACCTCTTCG CGCGAGGTGCC CGGTGGGCC	CGGGGGCGCG	1980
CGATGGGAA TTC		1993

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

DPEP

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACCA	ATCACCATCA	CATGACATAG	GTCGACCCCA	ACTTGACACGG	TGCGAACGGGA	50
CGATTGGGG	CACTGGGG	CGCGCGGG	GGCGGGGG	GCTTGGGTGAC	CGTTGGGGGTC	120
CCCGCGACCG	CCACCGCGCA	TCCGAGGCCA	GGCGCCCCGG	TACCCACAAAC	GGCGGCCCTCG	180
CGCGCGCTGA	CGCGCTGACG	GGCACCGCGC	CGCGCGACAC	CTGTTGGCGG	CCACCCACCG	240
GGCGCGCGCA	ACAGCGCGCA	TGGCAGCGG	GGCGATCCCA	ACGCGACACC	TCCGCGCGGC	300
GGCCGCGACG	CGCGCGCGGG	ACTTGTGAT	GGCGCAACCG	CAACCCACCC	TGTCGGGATC	360
GACACCGGG	TTGGAGGATT	CAAGCTTGG	CTGGCTGCTG	GCTGGGTGGG	GTCTGACGCC	420
GGCCACTTCG	ACTACGGTTG	ACATACCTTC	AGCAAAACCA	CGGGGGACCC	GCCATTTC	480
GGACAGCGCG	CGCGGGTGGC	CAATGACACC	CTGATCTG	TGCGCGCGGT	AGACCAAAAG	540
CTTAACTCCA	GGCGCGAAGG	CAACGACCTC	ARGGGCGGGG	CCGGGTTGGG	CTGGGACATG	600
GGTAGTCTT	ATATGCGCTA	CCGGGGCACC	CGGATCAACC	AGGAAAACCGT	CTCGCTCGAC	660
GCGACCGGG	TUTCTGGTAA	TCTGGTGTATA	TAGGAACTCA	AGTTGAGCGA	TUCGGAGTAC	720
CGGAAACGGG	AGATCTGGAC	GGCGTGTATA	GGCTGGCGG	CGCGGAACCC	ACCGGACGCC	780
GGGGCGCGTC	AGGCGCTGGT	TGTGTTGTTG	CTGGGGACCC	CAACACACCC	GTTGGACAG	840
GGCGCGCGCA	GGGCGCTGGC	CGAATGCGG	GGCGTTTGTG	TGCGCGCGGC	GGCGCGCGCG	900
GCACCGGGTC	CTGCAAGAGCC	CGCTACGGGG	CGGGCGCGGG	CGGGGGAACT	CGCTCTTACC	960
CGACGACAC	CGACACCCCA	CGGGACCTTA	CGGGCGCTGA			999

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His Met His Cln Val Asp Pro Asn Leu Thr
 1 3 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Ala Ile Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160
 Gly Gin Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175
 Leu Asp Gla Lys Leu Tyr Ala Ser Ala Gla Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gin Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

TbH4

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCGG ATTGGCGGGG TTTCGCCACC

CGAGGAAAGC CCGTACCAAGA TGGCGCTSCC GAAAGTAGGGC GATCCGTTGC CGATGCCGC 120
 ATGAAACGGGC GGCHTCAAAT TAGTGCAAGG ACCTTTCACTG TTAGCGACGCA TAATGGCTAT 180
 AGCACTAAGG AGGTGATTCG GATATGACGAC AGTGCAGACG CTGACCGGTG GATCAGCRAG 240
 AGATTTGAA CAGGGCCCAAC GAGGTTGAAGG CCCCCGAGGC GGACCCACCC ACTGATGTCG 300
 CCATCACACC GTGCGAACTC ACGGNGGWTAA AAAACGCCGC CCAACAGNTG GATTTGTCGG 360
 CGQACAACTAT CGGGGATTCG CTGGCCAAAGA CGGGCAGCGT CTGGGCAAGCT CTGGUGACCT 420
 CGCTCGCGCA CGGGGCCAAG GNGTATGGCG AGGTGATGTA CGGAGGCTCGG AGCGGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCGG AATCGGCGCG GGGCGTGGGA GGGGACAGTT 540
 CGGGCGAAGT AACCGATACG CGGAGGGCTGG CCACGGCGCG TGAAACCCAAC TTCTATGGATC 600
 TCAAAAGAAGC CGCAGGAAAG CTGGAAACCG CGGACCRAGG CGCATCGCTC CGGCACTONQ 660
 CGGATGGTG CGAACCTCTG ACCTGACCGC TGCAAGGCGA CG 720

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val
1															
															15
Lys															
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln
20															
															30
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val	
35															
															45
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu
50															
															60
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	
65															
															80
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	
85															
															95
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala
100															
															110
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Kaa	Gln	Ile	Leu	Ala	Ser	Gly	Val
115															
															125
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
130															
															140
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
145															
															160
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
165															
															175
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
180															
															190
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Ile	
195															
															205
Arg	Pro	Trp	Val	Phe	Gly	Thr	Tyr	Leu	Thr	Gly	Asp	Gly	Phe		
210															
															220
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
225															
															240
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Thr	Pro	Gly	Arg
245															
															255
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
260															
															270
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Lys	Leu	Arg	Pro	Xaa	Lys		

378

230

385

MThRa12

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x4) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTAAAGAAC	ACGGCGGCGT	CCGATTAACCT	CCAGCTGTCC	CAGGGTGKGC	AGGGATTGCG	60
CTTCCCGATC	GGGCAAGCGA	TGCGATAGCG	GGGCCAGATG	CGATCGGGGT	GGGGTCACCC	120
CACCCCTCAT	ATCGGGGCTA	CGCGCTTCT	CGCTTGTGGT	GTGTGCGACA	ACACCGCAA	180
CGGGCAGCAC	GTCCACAGCCG	TGTTGGGGCG	CGCTCGCGG	CGATCTCTCG	CGATCTCCAC	240
CGGGTACGTC	ATACACCGCG	TGAGACGGCG	TGGATCAAC	TGGGCCACCG	CGATGGCGGA	300
CGCGCTTAAC	GGGCATCAATC	CGCGTACCG	CGATCTCGGTG	AACTGGCGAA	CGACATGCGG	360
CGGGACCGCT	ACAGCGGAAACG	TGACATGCGC	CGAGGGACCC	CGGGCTCTGAT	TGCTGCGYGG	420
ATACCAACCG	CGGGCGGGCC	ATATGGA				480

(2) INFORMATION FOR SEO ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:66:

121 INFORMATION FOR SSO NO NO: 240:

THE SOURCELESS CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAGTTGAA	AGTTTGTCTG	CCTGAGTACT	GGCGATACTGG	GTTGTCGAGC	GGCGCTTGCG	50
TTTCTCTGCT	CGGTTTCCGAG	CGACAGCTAA	CTTGACCGCC	ATTAAGCGGAA	CATTACGAA	120
GGCTATTTGCC	CGGGTGTGGCG	ATGGGGTTT	GGGGACTTGG	CCCTGTCGCA	GGGGCGAAG	180
TACCCCGACG	GCTCGTTTG	SCAACCTGG	ATGCAACATG	GTTTACCGG	CCACAGTET	240
TACTCTGAAT	GTGTCGACGG	CGGTGAGGCC	CTTCCCCGCC	GGCCGCCACC	GGTGTGGTTGC	300
CGGGCGGAA	TTTCGCTCGGA	GGACGCCGAC	GCTCCCTGTG			339

(2) INFORMATION FOR SEC ID NO: 242

(ii) SENTENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

first MOLECULE TYPE: protein

(x) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1 5 10 15
 Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 20 25 30
 Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35 40 45
 Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50 55 60
 Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65 70 75 80
 Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
 85 90 95
 Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
 100 105 110

ESAT-6

(2) INFORMATION FOR SEQ ID NO:103:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC ACGAGTGGAA TTTCGGCGGT ATCGAAGGCC CGGCAAGCGC ATGCCAGGGA	60
AATGTCAGCT CCATTCATTC CCTCTCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA	120
CCGGCTCTGGC CGCGTAGCCG TTCCGAAAGCG TACCG	154

(xii) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Glu Glu Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser	
1	
	5
	10
	15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly	
20	
	25
	30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser	
35	
	40
	45
Glu Ala Tyr	
50	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/25008**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) A61K 39/005, 39/08, 39/00; C07K 1/00;
 US CL 435/240.1, 234.1, 185.1, 190.1, 199.1, 430/350.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/240.1, 234.1, 185.1, 190.1, 199.1, 430/350.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	WO 99/51748 A2 (CORIXA CORPORATION) 14 October 1999, see entire document.	18-28 and 72-79
Y, P	HENDRICKSON et al. Mass spectrometric identification of Mtb81, a novel serological marker for tuberculosis. J. Clin. Microbiol. June 2000, Vol. 38, No. 6, pages 2354-2361, see entire document.	1-3, 18-28, 56-58 and 72-79
Y, P	BRANDT et al. ESAT-6 subunit vaccination against Mycobacterium tuberculosis. Infect. Immun. February 2000, Vol. 68, No. 2, pages 791-795, see entire document.	18-28 and 72-79

Further documents are listed in the continuation of Box C. See parent family annex.

Special categories of cited documents	-P-	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A	-N*	document defining the general state of the art which is not considered to be of particular relevance
B	-E*	earlier document published at or after the international filing date document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified)
C	-V*	document referring to an oral disclosure, use, exhibition or other means
D	-V*	document published prior to the international filing date but later than the priority date claimed

Date of the actual completion of the international search Date of mailing of the international search report

26 DECEMBER 2000

06 FEB 2001

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20234 Facsimile No. (703) 506-5280	Authorized officer S. DEVIA, R.D. <i>George Bridger Jr.</i> Telephone No. (703) 506-0906
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/28095

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y, P	ALDERSON et al. Expression cloning of an immunodominant family of <i>Mycobacterium tuberculosis</i> antigens using human CD4+ T cells. <i>J. Exp. Med.</i> 07 February 2000, Vol. 191, No. 3, pages 551-559, see entire document.	18-28 and 72-79
Y	COLER et al. Molecular cloning and immunologic reactivity of a novel low molecular mass antigen of <i>Mycobacterium tuberculosis</i> . <i>J. Immunol.</i> 01 September 1998, Vol. 161, No. 5, pages 2366-2364, see entire document.	18-28 and 72-79
Y	ZIMMERMAN et al. Immunization with peptide heteroconjugates primes a T helper cell type 1-associated antibody (IgG2a) response that recognizes the native epitope on the 38-kDa protein of <i>Mycobacterium tuberculosis</i> . <i>Vaccine Res.</i> 1996, Vol. 5, No. 2, pages 103-118, see entire document.	18-28 and 72-79
Y	LEAO et al. Immunological and functional characterization of proteins of the <i>Mycobacterium tuberculosis</i> antigen 85 complex using synthetic peptides. <i>J. Gen. Microbiol.</i> 1993, Vol. 139, pages 1543-1549, see entire document.	18-28 and 72-79
Y	VORDERMEIER et al. Synthetic delivery system for tuberculosis vaccines: immunological evaluation of the <i>M. tuberculosis</i> 38 kDa protein entrapped in biodegradable PLG microparticles. <i>Vaccine</i> 1995, Vol. 13, No. 16, pages 1576-1582, see entire document.	18-28 and 72-79
Y	LOWRIE et al. Progress towards a new tuberculosis vaccine. <i>BioDrugs</i> September 1998, Vol. 10, No. 3, pages 201-213, see entire document.	18-28 and 72-79

INTERNATIONAL SEARCH REPORT

<p>International application No. PCT/US00/99088</p>

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-3, 18-28, 56-58 and 72-79.

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/08895

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used)

DIALOG, MEDLINE, EMBASE, WEST, BIOSIS, PASCAL.

Mycobacter, Mtb, MTB81, TbRas, zdkD, Tbs8-1, MTb81, FL TbH4, HTCC#1, Mtb40, TbH9, MTCC#4, MTb41, DPEP, DPPD, TbRas, TbRas1, MTb80, MTb81, Erdie, Mtb81, FL TbRas2, Mtb82, DPV, MTb8-4, MSL, MTbR8, MTI, MTb8-8A, MTI-A, ESAT-6, alpha-crystalline, ss complex.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 15.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-3 and 56-58, drawn to a pharmaceutical composition comprising a mycobacterial MTb81 antigen and an Mtb antigen and a method of eliciting an immune response by administering the same.

Group II, claims 4-6, 58-61, 107 and 108, drawn to a pharmaceutical composition comprising a mycobacterial TbRas, a ss 4D antigen, a Tb88-1 antigen and a FL TbH4 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group III, claims 7-14, 98-99 and 109-113, drawn to a pharmaceutical composition comprising a mycobacterial HTCC#1 and a TbH9 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group IV, claims 15-17, 69-71, 116 and 118, drawn to a pharmaceutical composition comprising a mycobacterial TbRas antigen and an HTCC#1 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group V, claims 80-82 and 80-83, an expression cassette comprising nucleic acids encoding mycobacterial MTb81 and Mtb antigens and a method of eliciting an immune response by administering the same.

Group VI, claims 88-89 and 88-87, drawn to an expression cassette comprising nucleic acids encoding mycobacterial TbRas, a ss 4D antigen, a Tb88-1 antigen and a FL TbH4 antigen and a method of eliciting an immune response by administering the same.

Group VII, claims 87-88 and 88-88, drawn to an expression cassette comprising nucleic acids encoding mycobacterial HTCC#1 and TbH9 antigen and a method of eliciting an immune response by administering the same.

Group VIII, claims 87-89 and 89-89, drawn to an expression cassette comprising nucleic acids encoding mycobacterial TbRas and HTCC#1 antigen and a method of eliciting an immune response by administering the same.

Claims 18-88 and 78-79 are considered linking claims and would be joined with one of inventions I, II, III and IV, if elected.

Claims 51-58 and 100-100 are considered linking claims and would be joined with one of inventions V, VI, VII and VIII, if elected.

The inventions listed as Groups I through VIII do not relate to a single inventive concept under PCT Rule 15.1 because, under PCT Rule 15.2, they lack the same or corresponding special technical features for the following reasons:

Inventions I through IV are drawn to compositions comprising distinct mycobacterial antigens and methods of using the same. Inventions V through VIII are drawn to four different expression cassettes and methods of using the same. Clearly, the special technical features of inventions I through VIII is not a unifying feature and there is no single general inventive concept underlying the plurality of claimed inventions of the present application in the sense of PCT Rule 15.1. Consequently, the application lacks unity of invention.